

APPROVED	C.G. FIG.	
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Systematic Gene Search in the Incyte LifeSeq Database

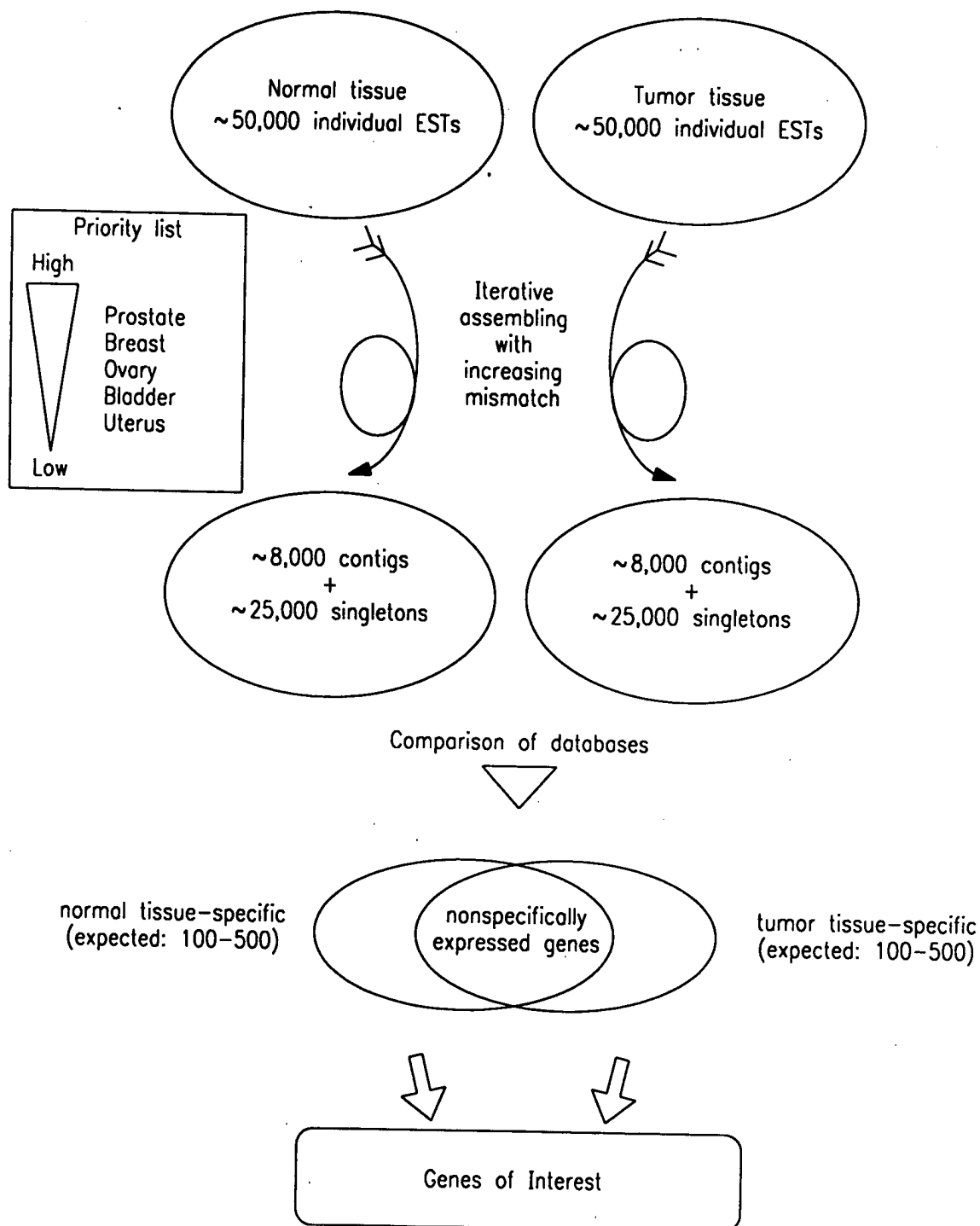
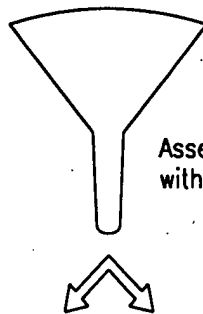


FIG. 1

Principle of EST Assembly

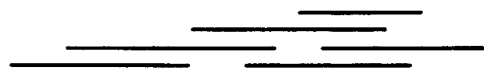
~50,000 ESTs per tissue



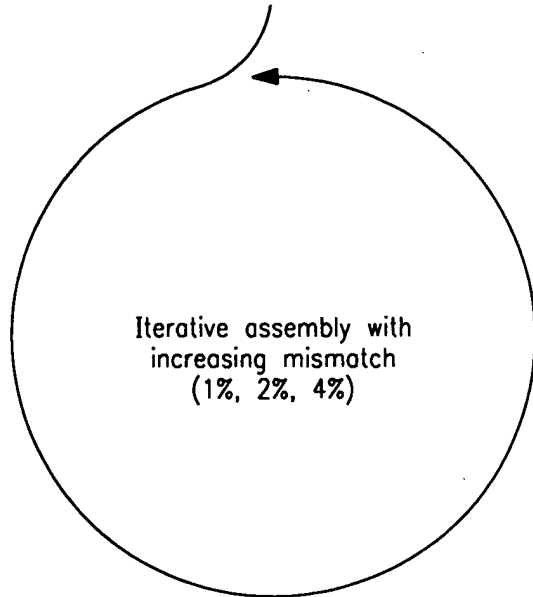
Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Singletons



Contigs increasing in
number and length



Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs ~25,000 other singletons



~30,000 consensus-
sequences per tissue

FIG. 2a

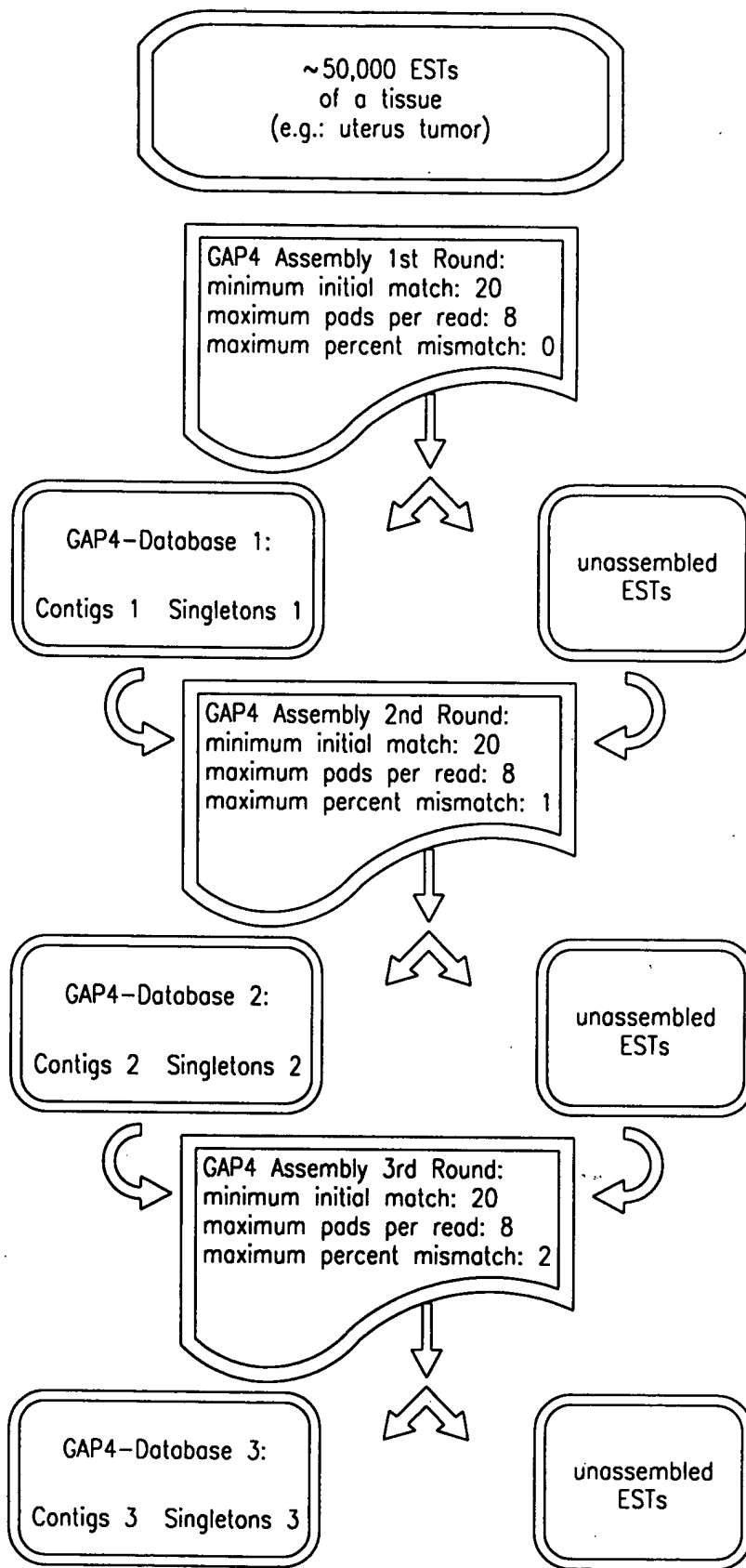


FIG. 2b-I

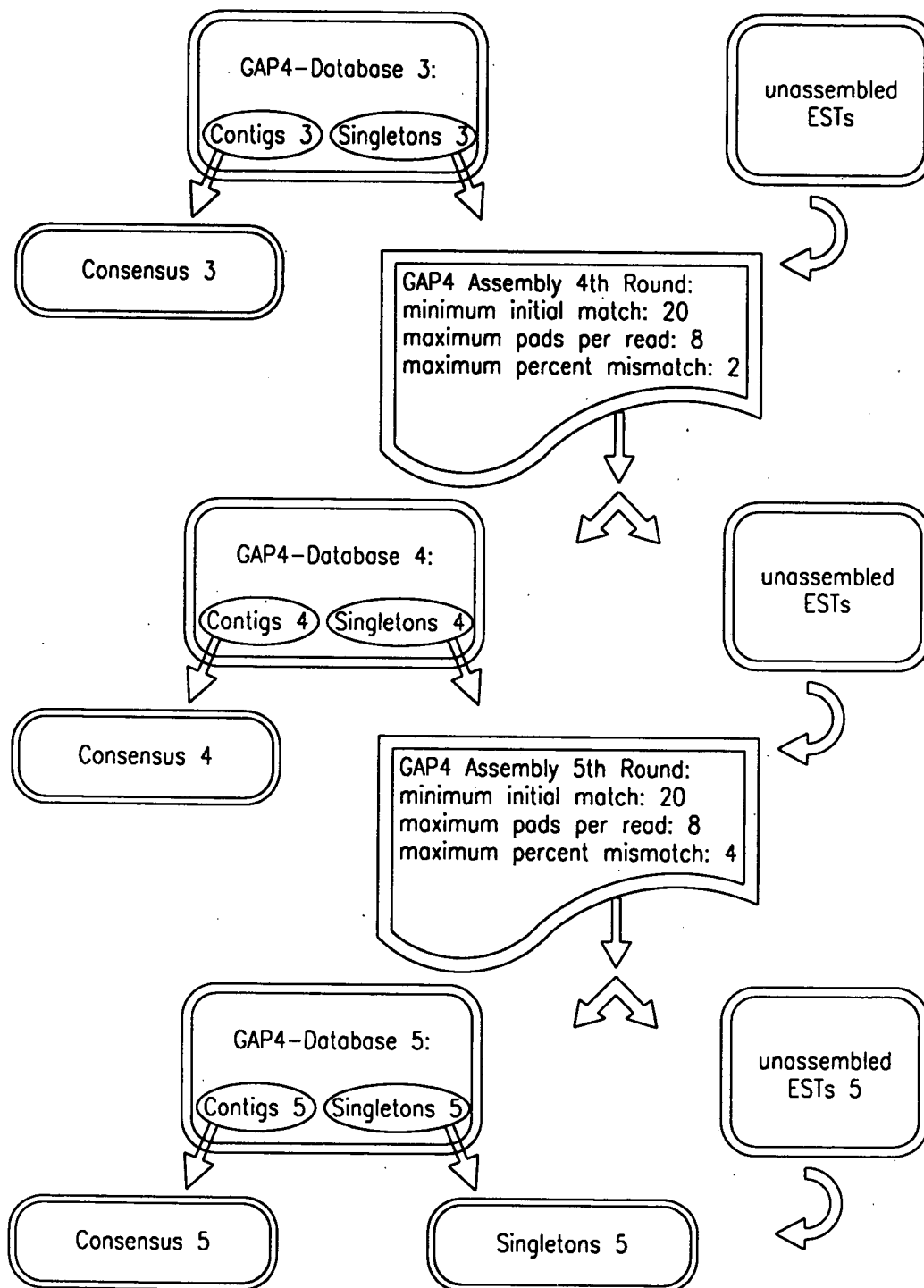


FIG. 2b-2

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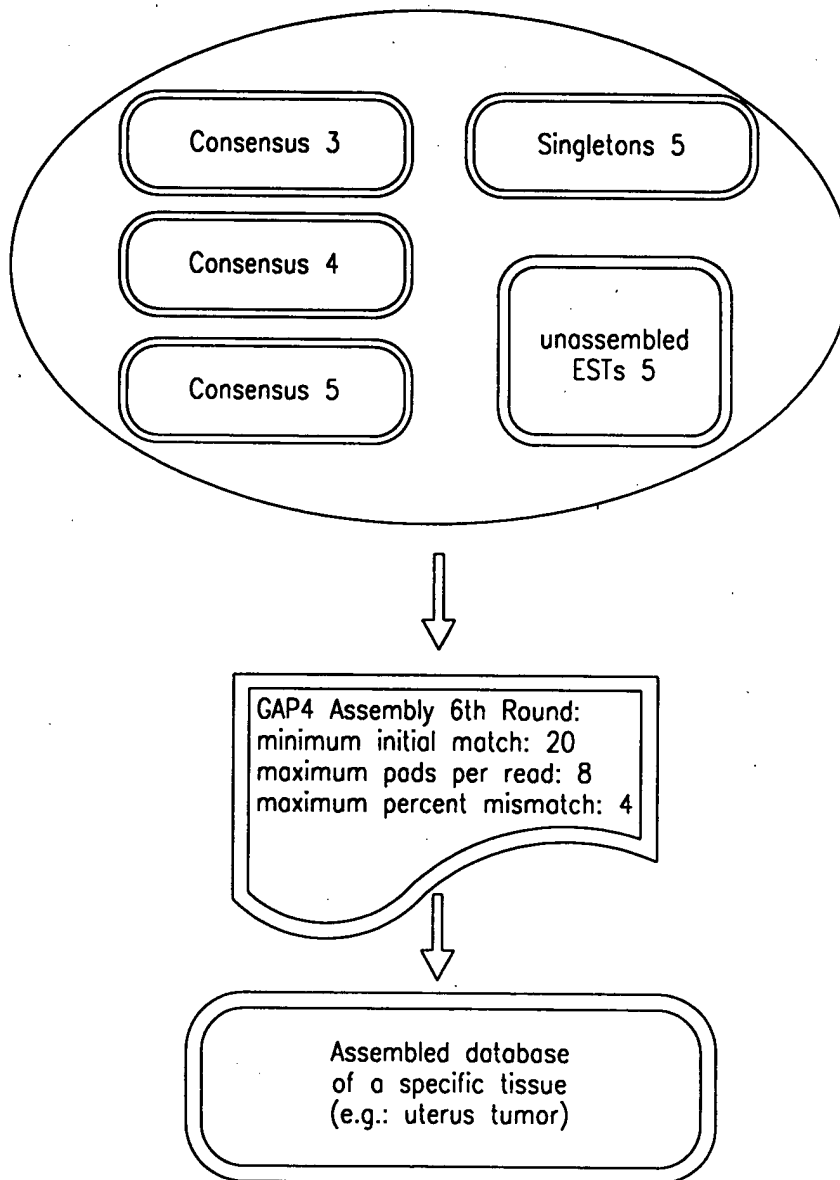


FIG. 2b-3

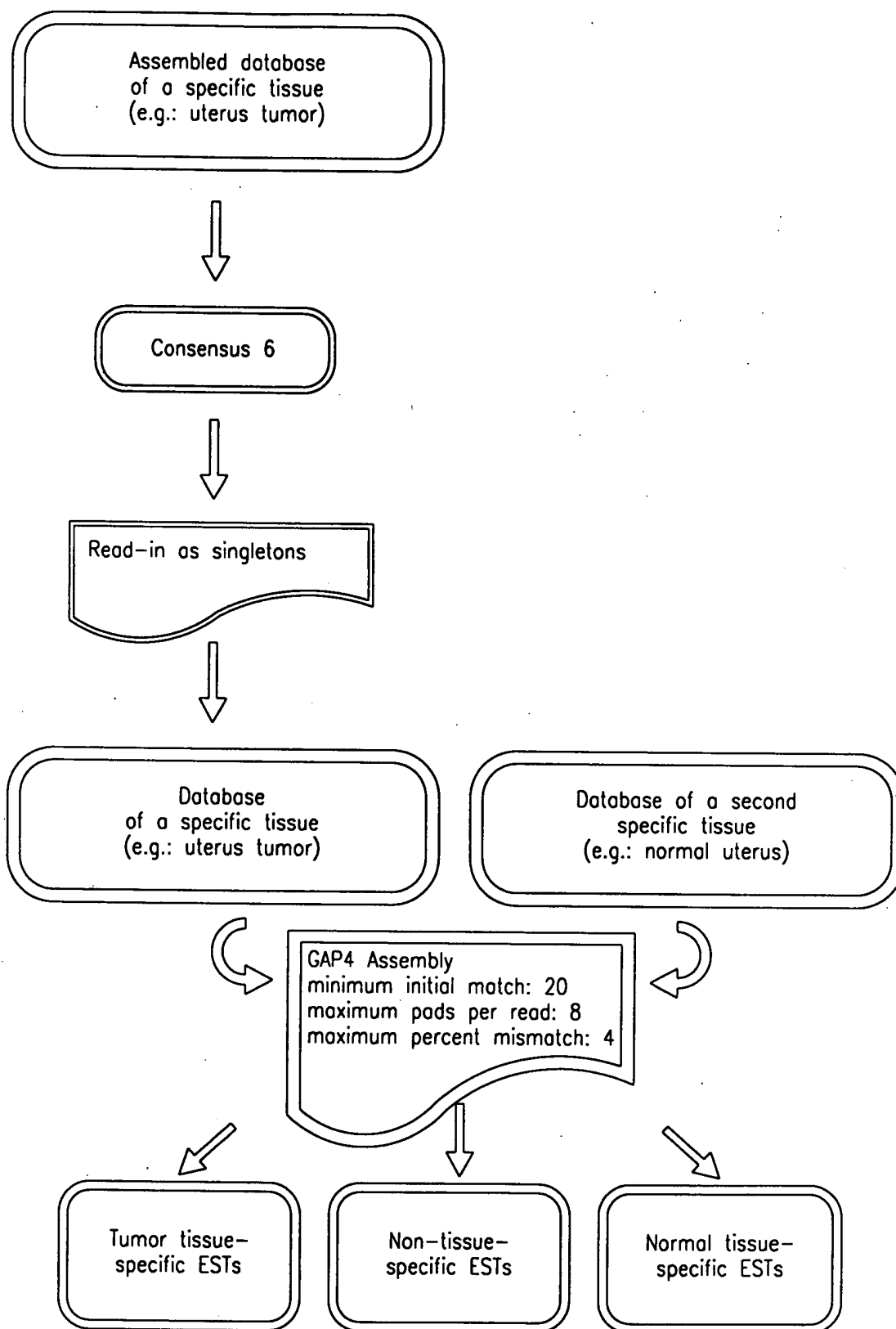


FIG. 2b-4

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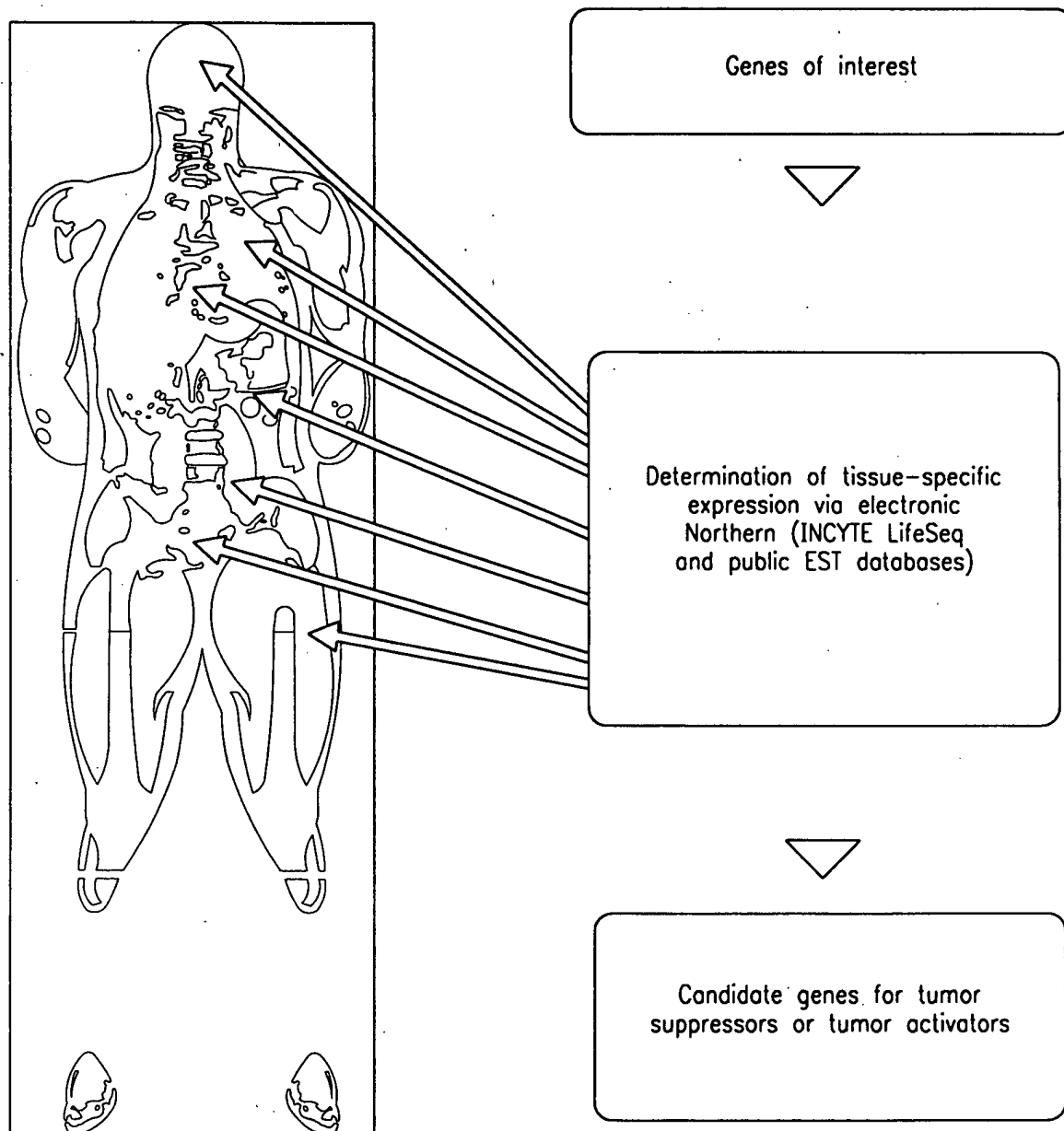


FIG. 4a

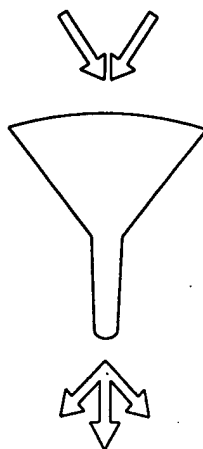
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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue



Assembly at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

FIG. 3

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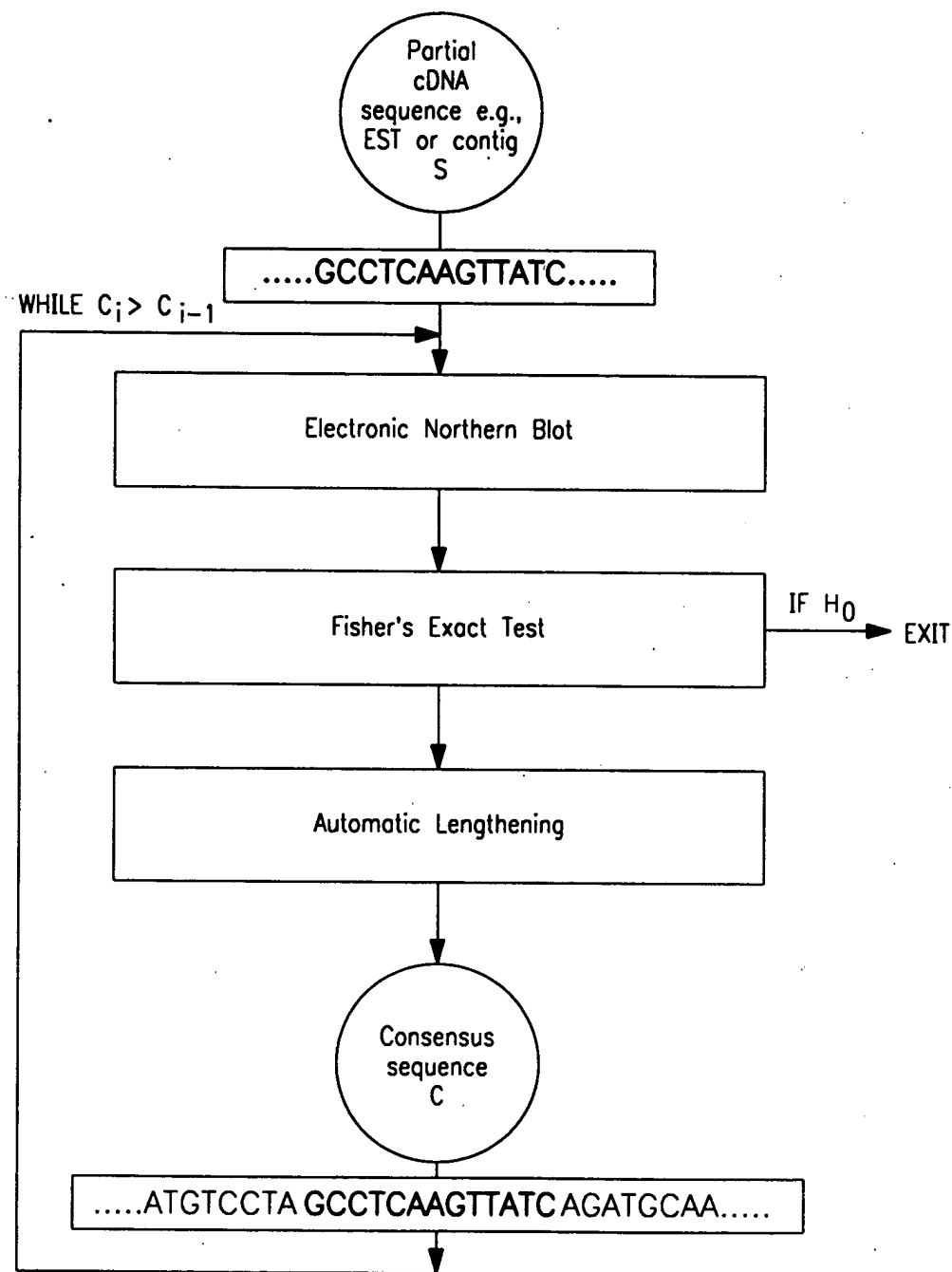


FIG. 4b

APPROVED	D.G. FIG.	
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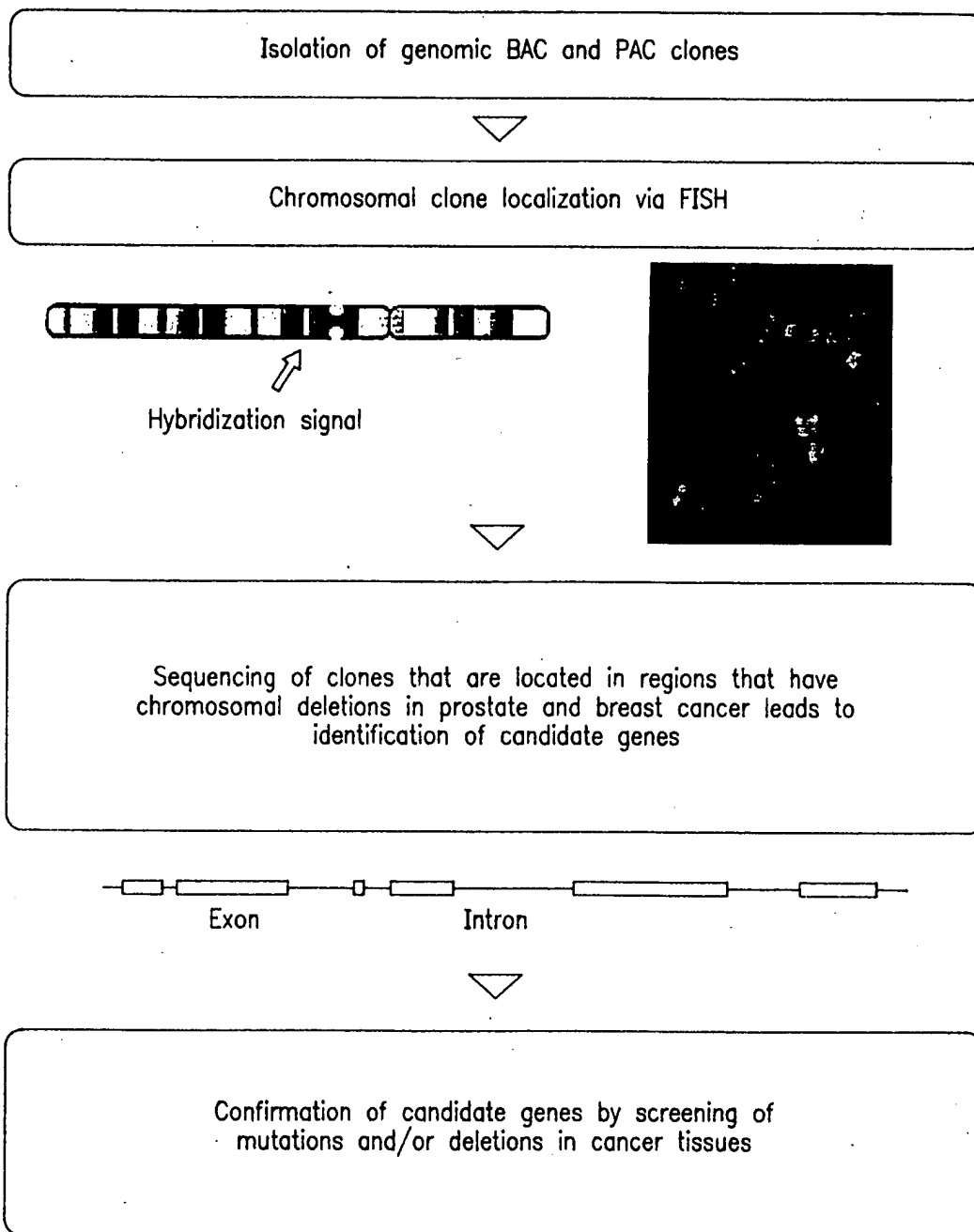


FIG. 5